

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
(A) NAME: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH
AND HUMAN SERVICES
(B) STREET: BOX OTT
(C) CITY: BETHESDA
(D) STATE OR PROVINCE: MARYLAND
(E) COUNTRY: UNITED STATES OF AMERICA
(F) POSTAL CODE: 20892
- (i) APPLICANT:
(A) NAME: PAVLAKIS, GEORGE N.
(B) STREET: 9 PURDUE COURT
(C) CITY: ROCKVILLE
(D) STATE OR PROVINCE: MARYLAND
(E) COUNTRY: UNITED STATES OF AMERICA
(F) POSTAL CODE: 20850
- (i) APPLICANT:
(A) NAME: FELBER, BARBARA K.
(B) STREET: 9 PURDUE COURT
(C) CITY: ROCKVILLE
(D) STATE OR PROVINCE: MARYLAND
(E) COUNTRY: UNITED STATES OF AMERICA
(F) POSTAL CODE: 20850
- (ii) TITLE OF INVENTION: METHOD OF ELIMINATING
INHIBITORY/INSTABILITY REGIONS OF mRNA
- (iii) NUMBER OF SEQUENCES: 130
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORGAN & FINNEGAN
(B) STREET: 345 PARK AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10154
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WORDPERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE: 02-MAY-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/050,478
(B) FILING DATE: 26-OCT-1994
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US93/02908
(B) FILING DATE: 29-MAR-1993
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/858,747
(B) FILING DATE: 27-MAR-1992
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: MORRY, MARY J.

(B) REGISTRATION NUMBER: 34,398
(C) REFERENCE/DOCKET NUMBER: 2026-4006US1

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212)758-4800
(B) TELEFAX: (212)751-6849

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 396 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTIONS:SEQ ID NO: 1:

ATGGGTGCGA GAGCGTCAGT ATTAAGCGGG GGAGAATTAG ATCGATGGGA AAAAATTCGG	60
TTAAGGCCAG GGGGAAAGAA AAAATATAAA TTTAAACATA TAGTATGGGC AAGCAGGGAG	120
CTAGAACGAT TCGCAGTTAA TCCTGGCCTG TTAGAACAT CAGAAGGCTG TAGACAAATA	180
CTGGGACAGC TACAACCATC CCTTCAGACA GGATCAGAAG AACTTAGATC ATTATATAAT	240
ACAGTAGCAA CCCTCTATTG TGTGCATCAA AGGATAGAGA TAAAAGACAC CAAGGAAGCT	300
TTAGACAAGA TAGAGGAAGA GCAAAACAAA AGTAAGAAAA AAGCACAGCA AGCAGCAGCT	360
GACACAGGAC ACAGCAATCA GGTCAGCCAA AATTAC	396

(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTIONS:SEQ ID NO: 2:

CCAGGGGGAA AGAAAAATA TAAATTAATA CATATAGTAT GGGCAAGCAG G	51
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(4) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTIONS:SEQ ID NO: 3:

CCTTCAGACA GGATCAGAAG AACTTAGATC ATTATATAAT ACAGTAGC	48
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(5) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTIONS:SEQ ID NO: 4:

ACCCTCTATT GTGTGCATCA AAGGATAGAG ATAAAAGACA CCAAGGAAGC	50
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(6) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTIONS: SEQ ID NO: 5:

GAGCAAAACA AAAGTAAGAA AAAAGCACAG CAAGCAGCAG CTGACACAGG

50

(7) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CCAGGGGGAA AGAAGAAGTA CAAGCTAAAG CACATCGTAT GGGCAAGCAG G

51

(8) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CCTTCAGACA GGATCAGAGG AGCTTCGATC ACTATACAAC ACAGTAGC

48

(9) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ACCCTCTATT GTGTGCACCA GCGGATCGAG ATCAAGGACA CCAAGGAAGC

50

(10) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GAGCAAAACA AGTCCAAGAA GAAGGCCAG CAGGCAGCAG CTGACACAGG

50

(11) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GAATAGTGCT GTTAACCTCC TGAACGCTAC CGCTATCGCC GTGGCGGAAG GAACCGACAG
GGTTATAG

60

68

(12) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

AAGTATTACA AGCCGCCTAC CGCGCCATCA GACATATCCC CGCCCGCATC CGCCAGGGCT
TG

60

62

(13) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GCTATAAGAT GGGCGGTAAA TGGAGCAAGT CCTCCGTCAT CGGCTGGCCT GCTGTAAG

58

(14) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGAAAGAATG CGCAGGGCCG AACCCGCCGC CGACGGAGTT GGCGCCGTAT CTCGAGAC

58

(15) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CTAGAAAAAC ACGGCGCCAT TACCTCCTCT AACACCGCCG CCAATAACGC CGCTTGTGCC
TG

60

62

(16) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GCTAGAAGCA CAGGAAGAAG AGGAAGTCGG CTTCCTCCGTT ACCCCTCAGG TACCTTTAAG

60

(17) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TGAAAACGTT CGCATGTGTC GCTACGTTGC TTACTAAGAT GGA

43

(18) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TTCTCAGATA CCTAGCTTCA TATTGCCTTA TTGTCTACCT TGA

43

(19) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GCCCTGTGAG TAGGCACTGA AGGACAGCCA TACGTAACAT ACAAGTGCCA

50

(20) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

AGCAGCAGCA ATGAACCTAG TAGCGATAGC CTGAGTAGCC CTACGCTGCT G

51

(21) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ACCCCGAGGC AGATAGCTTT CCATCCTGCG CTGCCGCTCA CCGCAAGGGC

50

(22) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CTGCACAGTG GAAGCCTCGG AATGGGCCCT ATGGCTACCG AATTGGAACC ACTGTGCACT C

61

(23) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CACCTAGAAC TTAAATGCA TGGGTAAAAG TAGTAGAAGA GAAGGCT

47

(24) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CACCTAGAAC CCTGAACGCC TGGGTGAAGG TGGTAGAAGA GAAGGCT

47

(25) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CCACCCACA AGATTAAAC ACCATGCTAA ACACAGTGGG GGGAC

45

(26) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CCACCCACA GGACCTGAAC ACGATGTTGA ACACCGTGGG GGGAC

45

(27) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CAGTAGGAGA AATTATAAA AGATGGATAA TCCTG

35

(28) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CAGTAGGAGA GATCTACAAG AGGTGGATAA TCCTG

35

(29) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GGATTAAATA AAATAGTAAG AATGTATAGC CCTACC

36

(30) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GGATTGAACA AGATCGTGAG GATGTATAGC CCTACC

36

(31) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

ACCGGTTCTA TAAACTCTA AGAGCCGAGC AAGCTTCACA G

41

(32) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ACCGGTTCTA CAAGACCCTG CGGGCTGAGC AAGCTTCACA G

41

(33) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

ATTGTAAGAC TATTTTAAAA GCATTGGGAC CAGCGGCTAC ACTA

44

(34) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

ATTGTAAGAC CATCCTGAAG GCTCTCGGCC CAGCGGCTAC ACTA

44

(35) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

AGAGTTTTGG CTGAAGCAAT GAGCCAAGTA ACAAATTCAG CTACCATAAT G

51

(36) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

AGAGTTTTGG CCGAGGCGAT GAGCCAGGTG ACGAACTCGG CGACCATAAT G

51

(37) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

CAGAGAGGCA ATTTTAGGAA CCAAAGAAAG ATTGTAAAGT GTTTC AATTG T

51

(38) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CAGAGAGGCA ACTTCCGGAA CCAGCGGAAG ATCGTCAAGT GTTCAATTG T

51

(39) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GAAGGGCACA CAGCCAGAAA TTGCAGGGCC CCTAGGAAAA AGGGCTGT

48

(40) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GAAGGGCACA CCGCCAGGAA CTGCCGGGCC CCCCAGGAAGA AGGGCTGT

48

(41) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

TGTGAAAGG AAGGACACCA AATGAAAGAT TGTACTGAGA GACAGGCTAA T

51

(42) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

TGTGAAAGG AGGGGCACCA GATGAAGGAC TGCACGGAGC GGCAGGCTAA T

51

(43) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CCCCTCGTCA CAATAAAGAT AGGGGGGCAA CTAAAGGAAG CTCTATTAGA TACAGGAG

58

(44) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CCCCTCGTCA CAGTAAGGAT CGGGGGGCAA CTCAAGGAAG CGCTGCTCGA TACAGGAG

58

(45) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GATAGGGGGA ATTGGAGGTT TTATCAAAGT AAGACAGTAT GATCAGATAC TC

52

(46) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GATAGGGGGG ATCGGGGGCT TCATCAAGGT GAGGCAGTAC GACCAGATAC TC

52

(47) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

CCTATTGAGA CTGTACCAGT AAAATTAAAG CCAGGAATGG ATGGCCCA

48

(48) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CCTATTGAGA CGGTGCCCGT GAAGTTGAAG CCGGGGATGG ATGGCCCA

48

(49) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 BASE PAIRS

(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

CAATGGCCAT TGACAGAAGA AAAAATAAAA GCATTAGTAG AAATTTGTAC AGAGA

55

(50) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

CAATGGCCAT TGACGGAAGA GAAGATCAAG GCCTTAGTCG AAATCTGTAC AGAGA

55

(51) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

TTCAGGAAGT ATACTGCATT TACCATACCT AGTATAACA ATGAGACACC A

51

(52) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

TTCAGGAAGT ACACGGCGTT CACCATCCCG AGCATCAACA ACGAGACACC A

51

(53) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

TTAGTGGGGA AATTGAATTG GGCAAGTCAG ATTTACCCAG GGATTAAAG

49

(54) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

TTAGTGGGGA AGGTGAACTG GCGAGCCAG ATCTACCCGG GGATTAAAG

49

(55) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GGCCAATGGA CATATCAAAT TTATCAAGAG CCATTAAAA ATCTGAAAAC AGG

53

(56) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GGCCAATGGA CGTACCAGAT CTACCAGGAG CCGTTCAAGA ACCTGAAAAC AGG

53

(57) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TGGGGAAAGA CTCCTAAATT TAACTGCCC ATACAAAAGG AAACATGGG

49

(58) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TGGGGAAAGA CGCCGAAGTT CAAGCTGCCC ATCCAGAAGG AGACATGGG

49

(59) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GAAGACTGAG TTACAAGCAA TTTATCTAGC TTTGCAGGAT TCGGGATTAG

50

(60) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GAAGACTGAG CTGCAGGCGA TCTACCTGGC GCTGCAGGAC TCGGGATTAG

50

(61) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GTTAGTCAAT CAAATAATAG AGCAGTTAAT AAAAAAGGAA AAGGTCTATC TGGCAT

56

(62) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GTTAGTCAAC CAAATCATCG AGCAGCTGAT CAAGAAGGAG AAGGTGTATC TGGCAT

56

(63) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GTCAGTGCTG GAATCAGGAA AGTACTATTT TTAGATGGAA TAGATAAGGC CC

52

(64) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GTCAGTGCTG GGATCCGGAA GGTGCTATTC CTGGACGGGA TCGATAAGGC CC

52

(65) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GAACATGAGA AATATCACAG TAATTGGAGA GCAATGGCTA GTGATTTTAA CCTGCCAC

58

(66) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GAACATGAGA AGTACCACTC CAACTGGCGC GCTATGGCCA GCGACTTCAA CCTGCCAC

58

(67) INFORMATION FOR SEQ ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GGAATATGGC AACTAGATTG TACACATTGA GAAGGAAAAG TTATCCTGGT AG

52

(68) INFORMATION FOR SEQ ID NO: 67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GGAATATGGC AGCTGGACTG CACGCACCTG GAGGGGAAGG TGATCCTGGT AG

52

(69) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

GCAGAAGTTA TTCCAGCAGA AACAGGGCAG GAAACAGCAT ATTTCTTTT AAAATTAGCA

60

GGAAGA

66

(70) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GCAGAAGTTA TCCCTGCTGA AACTCGGCAG GAGACCGCCT ACTTCCTGCT CAAACTCGCA

60

GGAAGA

66

(71) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

TGGCCAGTAA AAACAATACA TACTGACAAT GGCAGCAATT TCACCGGTGC TACGG

55

(72) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

TGGCCAGTGA AGACGATCCA CACGGACAAC GGAAGCAACT TCACTGGTGC TACGG

55

(73) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

GGAGTAGTAG AATCTATGAA TAAAGAATTA AAGAAAATTA TAGGACAGGT AA

52

(74) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

GGAGTAGTAG AATCCATGAA CAAGGAACTG AAGAAGATCA TCGGACAGGT AA

52

(75) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

TGGCCAGTAA AAACAATACA CACGGACAAC GGAAGCAACT TCACTGGTGC TACGG

55

(76) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 BASE PAIRS

(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CTTGGGATGT TGATGATCTG TAGTGCTACA GAAAAATTGT GGGTC

45

(77) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CTTGGGATGC TGATGATCTG CAGCGCCACC GAGAAGCTGT GGGTC

45

(78) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

ATTATGGGGT ACCTGTGTGG AAG

23

(79) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

ATTATGGCGT GCCCGTGTGG AAG

23

(80) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

CACCTATTT TGTGCATCAG ATGCTAAAGC ATATGAT

37

(81) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

CACTCTATTC TCGCCTCCG ACGCCAAGGC ATATGAT

37

(82) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ACAGAGGTAC ATAATGTTTG GGCCAC

26

(83) INFORMATION FOR SEQ ID NO: 82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

ACAGAGGTGC ACAACGTCTG GGCCAC

26

(84) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CCAACCCACA AGAAGTAGTA TTGGTAAATG TGACAGAAAA TTTTAACATG TG

52

(85) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

CCAACCCCCA GGAGGTGGTG CTGGTGAACG TGACCGAGAA CTTCAACATG TG

52

(86) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

TAACCCCACT CTGTGTTAGT TTAAAGTGCA CTGATTTGAA GAATG

45

(87) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

TAACCCCTCTGCGTGAGCCTGAAGTGCA CCGACCTGAA GAATG

45

(88) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

ATCAGCACAA GCATAAGAGG TAAGGTGCAG

30

(89) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

ATCAGCACCA GCATCCGCGG CAAGGTGCAG

30

(90) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

GAATATGCAT TTTTTTATAA ACTTGATATA ATA

33

(91) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

GAATATGCCT TCTTCTACAA GCTGGATATA ATA

33

(92) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

CCAATAGATA ATGATACTAC CAGCTAT

27

(93) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CCAATAGCTA AGGACACCAC CAGCTAT

27

(94) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GCCCCGGCTG GTTTTGGGAT TCTAAATGT AATAATAAGA CGTTC

45

(95) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

GCCCCGGCCG GCTTCGGGAT CCTGAAGTGC AACAACAAGA CGTTC

45

(96) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CAACTGCTGT TAAATGGCAG TCTAGCAGAA GAAGAGGTAG TA

42

(97) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CAACTGCTGC TGAACGGCAG CCTGGCCGAG GAGGAGGTAG TA

42

(98) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

TCTGTCAATT TCACGGACAA TGCTAAAACC ATAAT

35

(99) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

TCTGCCAACT TCACCGACAA CGCCAAGACC ATAAT

35

(100) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CTGAACACAT CTGTAGAAAT TAATTGTACA AG

32

(101) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

CTGAACCACT CCGTGGAGAT CAACTGTACA AG

32

(102) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CAACAACAAT ACAAGAAAAA GAATCCGTAT C

31

(103) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

CAACAACAAC ACCGGCAAGC GCATCCGTAT C

31

(104) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

GCTAGCAAAT TAAGAGAACA ATTTGGAAAT AATAAAACAA TAATCTT

47

(105) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

GCTAGCAAGC TGC GCGAGCA GTACGGGAAC AACAAGACCA TAATCTT

47

(106) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

TTCTACTGTA ATTCAACACA ACTGTTTAAT AGTACTTGGT TTAAT

45

(107) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

TTCTACTGGA ACTCCACCCA GCTGTTCAAC AGCACCTGGT TTAAT

45

(108) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

CACAATCACC CTCCCATGCA GAATAAAACA AATTATAAAC ATG

43

(109) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CACAATCACC CTGCCCTGCC GCATCAAGCA GATCATAAAC ATG

43

(110) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CATCAGTGGG CAAATTAGAT GTTCATCAA TATTACAGGG CTGCTA

46

(111) INFORMATION FOR SEQ ID NO: 110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

CATCAGCGGC CAGATCCGCT GCTCCTCAA CATCACCGGG CTGCTA

46

(112) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

GAGGGACAAT TGGAGAAGTG AATTATATAA ATATAAAGTA GTAAAAATTG AACCATTA

58

(113) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

GAGGGACAAC TGGAGGAGCG AGCTGTACAA GTACAAGGTG GTGAAGATCG AACCATTA

58

(114) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

GCCTTGGAAT GCTAGTTGGA GTAATAAATC TCTGGAACAG

40

(115) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

GCCTTGGAAC GCCAGCTGGA GCAACAAGTC CCTGGAACAG

40

(116) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GAGTGGGACA GAGAAATTAA CAATTACACA AG

32

(117) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

GAGTGGGACC GCGAGATCAA CAACTACACA AG

32

(118) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATACACTCCT TAATTGAAGA ATCGCAAAAC CAGCAAGAAA AGAATGAA

48

(119) INFORMATION FOR SEQ ID NO: 118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

ATACACTCCC TGATCGAGGA GTCCGAGAAC CAGCAGGAGA AGAATGAA

48

(120) INFORMATION FOR SEQ ID NO: 119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

CAGGCCCGAA GGAATAGAAG AAGAAGGTGG AGAGAGAGAC

40

(121) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

CAGGCCCGAG GGCATCGAGG AGGAGGGCGG CGAGAGAGAC

40

(122) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

TACCACCGCT TGAGAGACTT ACTCTTGATT GTAACGAGGA TTGTGGAAC

50

(123) INFORMATION FOR SEQ ID NO: 122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

TACCACCGCC TCGCGACCT GCTCCTGATC GTGACGAGGA TCGTGGAAC

50

(124) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

GGTGGGAAGC CCTCAAATAT TGGTGGAATC TCCTACAGTA TTGG

44

(125) INFORMATION FOR SEQ ID NO: 124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

GGTGGGAGGC CCTCAAGTAC TGGTGAACC TCCTCCAGTA TTGG

44

(126) INFORMATION FOR SEQ ID NO: 125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

AGTCAGGAAC TAAAGAATAG TGCTGTTAGC TTGCTCAATG

40

(127) INFORMATION FOR SEQ ID NO: 126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

AGTCAGGAGC TGAAGAACAG CGCCGTGAAC CTGCTCAATG

40

(128) INFORMATION FOR SEQ ID NO: 127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

GGTACCAGCA CACAAAGGAA TTGGAGGAAA TGAACAAGTA GATAAATTAG TCAGTGCTGG
AATCAGGAAA GTACTATTTT TAGATGGAAT AGATAAGGCC CAAGATGAAC ATGAGAAATA
TCACAGTAAT TGGAGAGCAA TGGCTAGTGA TTTTAACCTG CCACCTGTAG TAGCAAAAGA
AATAGTAGCC AGCTGTGATA AATGTCAGCT AAAAGGAGAA GCCATGCATG GACAAGTAGA
CTGTAGTCCA GGAATATGGC AACTAGATTG TACACATTTA GAAGGAAAAG TTATCCTGGT
AGCAGTTCAT GTAGCCAGTG GATATATAGA AGCAGAAGTT ATTCCAGCAG AAACAGGGCA
GGAAACAGCA TATTTTCTTT TAA AATTAGC AGGAAGATGG CCAGTAAAAA CAATACATAC
TGACAATGGC AGCAATTTCA CCGGTGCTAC GGTTAGGGCC GCCTGTTGGT GGGCGGGAAT
CAAGCAGGAA TTTGG

60

120

180

240

300

360

420

480

495

(129) INFORMATION FOR SEQ ID NO: 128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7228 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

TGGAAGGGCT AATTTGGTCC CAAAAAGAC AAGAGATCCT TGATCTGTGG ATCTACCACA	60
CACAAGGCTA CTTCCCTGAT TGGCAGAACT ACACACCAGG GCCAGGGATC AGATATCCAC	120
TGACCTTTGG ATGGTGCTTC AAGTTAGTAC CAGTTGAACC AGAGCAAGTA GAAGAGGCCA	180
AATAAGGAGA GAAGAACAGC TTGTTACACC CTATGAGCCA GCATGGGATG GAGGACCCGG	240
AGGGAGAAGT ATTAGTGTGG AAGTTTGACA GCCTCCTAGC ATTTCGTAC ATGGCCCGAG	300
AGCTGCATCC GGAGTACTAC AAAGACTGCT GACATCGAGC TTTCTACAAG GGACTTTCCG	360
CTGGGGACTT TCCAGGGAGG TGTGGCCTGG GCGGGACTGG GGAGTGGCGA GCCCTCAGAT	420
GCTACATATA AGCAGCTGCT TTTTGCCTGT ACTGGGTCTC TCTGGTTAGA CCAGATCTGA	480
GCCTGGGAGC TCTCTGGCTA ACTAGGGAAC CCACTGCTTA AGCCTCAATA AAGCTTGCCT	540
TGAGTGCTCA AAGTAGTGTG TGCCCGTCTG TTGTGTGACT CTGGTAACTA GAGATCCCTC	600
AGACCCTTTT AGTCAGTGTG GAAAATCTCT AGCAGTGGCG CCCGAACAGG GACTTGAAAG	660
CGAAAGTAAA GCCAGAGGAG ATCTCTCGAC GCAGGACTCG GCTTGCTGAA GCGCGCGTCG	720
ACAGAGAGAT GGGTGCAGG GCGTCAGTAT TAAGCGGGGG AGAATTAGAT CGATGGGAAA	780
AAATTCGGTT AAGGCCAGGG GGAAAGAAGA AGTACAAGCT AAAGCACATC GTATGGGCAA	840
GCAGGGAGCT AGAACGATTC GCAGTTAATC CTGGCCTGTT AGAAACATCA GAAGGCTGTA	900
GACAAATACT GGGACAGCTA CAACCATCCC TTCAGACAGG ATCAGAGGAG CTTGATCAC	960
TATACAACAC AGTAGCAACC CTCTATTGTG TGCACCAGCG GATCGAGATC AAGGACACCA	1020
AGGAAGCTTT AGACAAGATA GAGGAAGAGC AAAACAAGTC CAAGAAGAAG GCCCAGCAGG	1080
CAGCAGCTGA CACAGGACAC AGCAATCAGG TCAGCCAAAA TTACCCTATA GTGCAGAACA	1140
TCCAGGGGCA AATGGTACAT CAGGCCATAT CACCTAGAAC TTTAAATGCA TGGGTAAAAG	1200
TAGTAGAAGA GAAGGCTTTC AGCCCAGAAG TGATACCCAT GTTTTCAGCA TTATCAGAAG	1260
GAGCCACCCC ACAGGACCTG AACACGATGT TGAACACCGT GGGGGGACAT CAAGCAGCCA	1320
TGCAATGTT AAAAGAGACC ATCAATGAGG AAGCTGCAGA ATGGGATAGA GTGCATCCAG	1380
TGCATGCAGG GCCTATTGCA CCAGGCCAGA TGAGAGAACC AAGGGGAAGT GACATAGCAG	1440
GAACTACTAG TACCCTTCAG GAACAAATAG GATGGATGAC AAATAATCCA CCTATCCCAG	1500
TAGGAGAGAT CTACAAGAGG TGGATAATCC TGGGATTGAA CAAGATCGTG AGGATGTATA	1560
GCCCTACCAG CATTCTGGAC ATAAGACAAG GACCAAAGGA ACCCTTTAGA GACTATGTAG	1620
ACCGGTTCTA TAAACTCTA AGAGCTGAGC AAGCTTCACA GGAGGTAAAA AATTGGATGA	1680
CAGAAACCTT GTTGGTCCAA AATGCGAACC CAGATTGTAA GACCATCCTG AAGGCTCTCG	1740
GCCCAGCGGC TACACTAGAA GAAATGATGA CAGCATGTCA GGGAGTAGGA GGACCCGGCC	1800
ATAAGGCAAG AGTTTTGTAG GGATCCACTA GTTCTAGACT CGAGGGGGGG CCCGGTACCT	1860
TTAAGACCAA TGACTTACAA GGCAGCTGTA GATCTTAGCC ACTTTTTAAA AGAAAAGGGG	1920
GGACTGGAAG GGCTAATTCA CTCCCAAAGA AGACAAGATA TCCTTGATCT GTGGATCTAC	1980
CACACACAAG GCTACTTCCC TGATTGGCAG AACTACACAC CAGGGCCAGG GGTGAGATAT	2040
CCACTGACCT TTGGATGGTG CTACAAGCTA GTACCAGTTG AGCCAGATAA GGTAGAAGAG	2100
GCCAATAAAG GAGAGAACAC CAGCTTGTTA CACCCTGTGA GCCTGCATGG AATGGATGAC	2160

CCTGAGAGAG AAGTGTTAGA GTGGAGGTTT GACAGCCGCC TAGCATTTC A TCACGTGGCC	2220
CGAGAGCTGC ATCCGGAGTA CTTCAAGAAC TGCTGACATC GAGCTTGCTA CAAGGGACTT	2280
TCCGCTGGGG ACTTTCAGG GAGGCGTGGC CTGGGCGGGA CTGGGGAGTG GCGAGCCCTC	2340
AGATGCTGCA TATAAGCAGC TGCTTTTTCG CTGTAAGTGG TCTCTCTGGT TAGACCAGAT	2400
CTGAGCCTGG GAGCTCTCTG GCTAACTAGG GAACCCACTG CTTAAGCCTC AATAAAGCTT	2460
GCCTTGAGTG CTTCAAGTAG TGTGTGCCCG TCTGTTGTGT GACTCTGGTA ACTAGAGATC	2520
CCTCAGACCC TTTTAGTCAG TGTGGAATAT CTCTAGCACC CCCCAGGAGG TAGAGGTTGC	2580
AGTGAGCCAA GATCGGCCA CTGCATTCCA GCCTGGGCAA GAAACAAGA CTGTCTAAAA	2640
TAATAATAAT AAGTTAAGGG TATTAAATAT ATTTATACAT GGAGGTCATA AAAATATATA	2700
TATTTGGGCT GGGCGCAGTG GCTCACACCT GCGCCCGGCC CTTTGGGAGG CCGAGGCAGG	2760
TGGATCACCT GAGTTTGGGA GTTCCAGACC AGCCTGACCA ACATGGAGAA ACCCCTTCTC	2820
TGTGTATTTT TAGTAGATTT TATTTTATGT GTATTTTATT CACAGGTATT TCTGAAAAAC	2880
TGAAACTGTT TTTCTCTAC TCTGATACCA CAAGAATCAT CAGCACAGAG GAAGACTTCT	2940
GTGATCAAAAT GTGGTGGGAG AGGGAGGTTT TCACCAGCAC ATGAGCAGTC AGTTCTGCCG	3000
CAGACTCGGC GGGTGTCTT CGGTTGAGT CCAACACCGC CTGCTGGAG AGAGGTCAGA	3060
CCACAGGGTG AGGGCTCAGT CCCCAGACA TAAACACCCA AGACATAAAC ACCCAACAGG	3120
TCCACCCCGC CTGCTGCCA GGCAGAGCCG ATTCACCAAG ACGGGAATTA GGATAGAGAA	3180
AGAGTAAGTC ACACAGAGCC GGCTGTGCGG GAGAACGGAG TTCTATTATG ACTCAAATCA	3240
GTCTCCCAA GCATTGGGG ATCAGAGTTT TTAAGGATAA CTTAGTGTGT AGGGGGCCAG	3300
TGAGTTGGAG ATGAAAGCGT AGGGAGTCGA AGGTGTCTT TTGCGCCGAG TCAGTTCTTG	3360
GGTGGGGGCC ACAAGATCGG ATGAGCCAGT TTATCAATCC GGGGGTGCCA GCTGATCCAT	3420
GGAGTGCAAG GTCTGCAAAA TATCTCAAGC ACTGATTGAT CTTAGGTTTT ACAATAGTGA	3480
TGTTACCCCA GGAACAATTT GGGGAAGGTC AGAATCTTGT AGCCTGTAGC TGCATGACTC	3540
CTAAACCATA ATTTCTTTTT TGTTTTTTTT TTTTATTTT TGAGACAGGG TCTCACTCTG	3600
TCACCTAGGC TGGAGTGCAG TGGTGCAATC ACAGCTCACT GCAGCCCTA GAGCGGCCGC	3660
CACCGCGGTG GAGCTCCAAT TCGCCCTATA GTGAGTCGTA TTACAATTCA CTGGCCGTCG	3720
TTTTACAAGC TCGTACTGG GAAAACCTG GCGTTACCCA ACTTAATCGC CTTGCAGCAC	3780
ATCCCCCTTT CGCCAGCTGG CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC	3840
AGTTGCGCAG CCTGAATGGC GAATGGCGCG AAATTGTAAA CGTTAATATT TTGTTAAAA	3900
TCGCGTTAAA TTTTGTAA ATCAGCTCAT TTTTAAACCA ATAGGCCGAA ATCGGCAAAA	3960
TCCCTTATAA ATCAAAAGAA TAGACCGAGA TAGGGTTGAG TGTTGTCCA GTTTGGAACA	4020
AGAGTCCACT ATTAAGAAC GTGGACTCCA ACGTCAAAGG GCGAAAAACC GTCTATCAGG	4080
GCGATGGCCC ACTACGTGAA CCATCACCTT AATCAAGTTT TTTGGGGTCG AGGTGCCGTA	4140
AAGCACTAAA TCGGAACCTT AAAGGGAGCC CCCGATTTAG AGCTTGACGG GGAAAGCCGG	4200
CGAACGTGGC GAGAAAGGAA GGAAGAAAG CGAAAGGAGC GGGCGCTAGG GCGCTGGCAA	4260

GTGTAGCGGT CACGCTGCGC GTAACCACCA CACCCGCCGC GCTTAATGCG CCGCTACAGG	4320
GCGCGTCCCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA ACCCCTATTT GTTTATTTTT	4380
CTAAATACAT TCAAATATGT ATCCGCTCAT GAGACAATAA CCCTGATAAA TGCTTCAATA	4440
ATATTGAAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT GTCGCCCTTA TTCCCTTTTT	4500
TGCGGCATTT TGCCCTTCTG TTTTGTCTCA CCCAGAAACG CTGGTGAAAG TAAAAGATGC	4560
TGAAGATCAG TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA GCGGTAAGAT	4620
CCTTGAGAGT TTTGCCCCG AAGAACGTTT TCCAATGATG AGCACTTTTA AAGTCTGCT	4680
ATGTGGCGCG GTATTATCCC GTATTGACGC CGGGCAAGAG CAACTCGGTC GCCGCATACA	4740
CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTCACA GAAAAGCATC TTACGGATGG	4800
CATGACAGTA AGAGAATTAT GCAGTGCTGC CATAACCATG AGTGATAACA CTGCGGCCAA	4860
CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAACC GCTTTTTTGC ACAACATGGG	4920
GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA TACCAAACGA	4980
CGAGCGTGAC ACCACGATGC CTGTAGCAAT GGCAACAACG TTGCGCAAAC TATTAAGTGG	5040
CGAACTACTT ACTCTAGCTT CCCGGCAACA ATTAATAGAC TGGATGGAGG CGGATAAAGT	5100
TGCAGGACCA CTTCTGCGCT CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG	5160
AGCCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG GGGCCAGATG GTAAGCCCTC	5220
CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC GAAATAGACA	5280
GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA CTGTCAGACC AAGTTTACTC	5340
ATATATACTT TAGATTGATT TAAAACTTCA TTTTAAATTT AAAAGGATCT AGGTGAAGAT	5400
CCTTTTTGAT AATCTCATGA CAAAATCCC TTAACGTGAG TTTTCGTTCC ACTGAGCGTC	5460
AGACCCCGTA GAAAAGATCA AAGGATCTTC TTGAGATCCT TTTTCTGTC GCGTAATCTG	5520
CTGCTTGCAA AAAAAAAC CACCGCTACC AGCGGTGGTT TGTGCGCG ATCAAGAGCT	5580
ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG CAGATACCA ATACTGTCCT	5640
TCTAGTGTAG CCGTAGTTAG GCCACCACTT CAAGAACTCT GTAGCACCGC CTACATACCT	5700
CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG	5760
GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA CGGGGGGTTT	5820
GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC TACAGCGTGA	5880
GCTATGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGCG GACAGGTATC CGGTAAGCGG	5940
CAGGGTCGGA ACAGGAGAGC GCACGAGGGA GCTTCCAGGG GGAACGCCT GGTATCTTTA	6000
TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA TTTTGTGAT GCTCGTCAGG	6060
GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCGGCCTTT TTACGGTTCC TGCCCTTTTG	6120
CTGGCCTTTT GCTCACATGT TCTTTCCTGC GTTATCCCCT GATTCTGTGG ATAACCGTAT	6180
TACCGCCTTT GAGTGAGCTG ATACCGCTCG CCGCAGCCGA ACGACCGAGC GCAGCGAGTC	6240
AGTGAGCGAG GAAGCGGAAG AGCGCCCAAT ACGCAAACCG CCTCTCCCCG CGCGTTGGCC	6300
GATTCAATTA TGCAGCTGGC ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA	6360
CGCAATTAAT GTGAGTTAGC TCACTCATTA GGCACCCAG GCTTTACACT TTATGCTTCC	6420

GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA ACAGCTATGA	6480
CCATGATTAC GCCAAGCTCG GAATTAACCC TCACTAAAGG GAACAAAAGC TGCTGCAGGG	6540
TCCCTAACTG CCAAGCCCCA CAGTGTGCCC TGAGGCTGCC CCTTCCTTCT AGCGGCTGCC	6600
CCCCTCGGC TTTGCTTTCC CTAGTTTCAG TTACTTGCGT TCAGCCAAGG TCTGAAACTA	6660
GGTGCACACA GAGCGGTAAG ACTGCGAGAG AAAGAGACCA GCTTTACAGG GGGTTTATCA	6720
CAGTGCACCC TGACAGTCGT CAGCCTCACA GGGGGTTTAT CACATTGCAC CCTGACAGTC	6780
GTCAGCCTCA CAGGGGGTTT ATCAGAGTGC ACCCTTACAA TCATTCCATT TGATTCACAA	6840
TTTTTTTAGT CTCTACTGTG CCTAACTTGT AAGTTAAATT TGATCAGAGG TGTGTTCCCA	6900
GAGGGGAAAA CAGTATATAC AGGGTTCAGT ACTATCGCAT TTCAGGCCCTC CACCTGGGTC	6960
TTGGAATGTG TCCCCGAGG GGTGATGACT ACCTCAGTTG GATCTCCACA GGTGACAGTG	7020
ACACAAGATA ACCAAGACAC CTCCAAGGC TACCACAATG GGCCGCCCTC CACGTGCACA	7080
TGGCCGGAGG AACTGCCATG TCGGAGGTGC AAGCACACCT GCGCATCAGA GTCCTTGGTG	7140
TGGAGGGAGG GACCAGCGCA GCTTCCAGCC ATCCACCTGA TGAACAGAAC CTAGGGGAAAG	7200
CCCCAGTTCT ACTTACACCA GGAAAGGC	7228

(130) INFORMATION FOR SEQ ID NO: 129

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7228 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

TGGAAGGGCT AATTGGTCC CAAAAAGAC AAGAGATCCT TGATCTGTGG ATCTACCACA	60
CACAAGGCTA CTTCCTGAT TGGCAGAACT ACACACCAGG GCCAGGGATC AGATATCCAC	120
TGACCTTTGG ATGGTGCTTC AAGTTAGTAC CAGTTGAACC AGAGCAAGTA GAAGAGGCCA	180
AATAAGGAGA GAAGAACAGC TTGTACACC CTATGAGCCA GCATGGGATG GAGGACCCGG	240
AGGGAGAAGT ATTAGTGTGG AAGTTTGACA GCCTCCTAGC ATTCGTCAC ATGGCCCGAG	300
AGCTGCATCC GGAGTACTAC AAAGACTGCT GACATCGAGC TTTCTACAAG GGACTTTCCG	360
CTGGGGACTT TCCAGGGAGG TGTGGCCTGG GCGGGACTGG GGAGTGGCGA GCCCTCAGAT	420
GCTACATATA AGCAGCTGCT TTTGCCTGT ACTGGGTCTC TCTGGTTAGA CCAGATCTGA	480
GCCTGGGAGC TCTCTGGCTA ACTAGGGAAC CCACTGCTTA AGCCTCAATA AAGCTTGCCT	540
TGAGTGCTCA AAGTAGTGTG TGCCCGTCTG TTGTGTGACT CTGGTAACTA GAGATCCCTC	600
AGACCCTTTT AGTCAGTGTG GAAAATCTCT AGCAGTGGCG CCCGAACAGG GACTTGAAAG	660
CGAAAGTAAA GCCAGAGGAG ATCTCTCGAC GCAGGACTCG GCTTGCTGAA GCGCGCGTCG	720
ACAGAGAG ATG GGT GCG AGA GCG TCA GTA TTA AGC GGG GGA GAA TTA GAT	770
Met Gly Ala Ser Val Leu Ser Gly Gly Glu Leu Asp	
1 5 10	
CGA TGG GAA AAA ATT CGG TTA AGG CCA GGG GGA AAG AAG TAC AAG	818
Arg Trp Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys	
15 20 25 30	

CTA AAG CAC ATC GTA TGG GCA AGC AGG GAG CTA GAA CGA TTC GCA GTT Leu Lys His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val 35 40 45	866
AAT CCT GGC CTG TTA GAA ACA TCA GAA GGC TGT AGA CAA ATA CTG GGA Asn Pro Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly 50 55 60	914
CAG CTA CAA CCA TCC CTT CAG ACA GGA TCA GAG GAG CTT CGA TCA CTA Gln Leu Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu 65 70 75	962
TAC AAC ACA GTA GCA ACC CTC TAT TGT GTG CAC CAG CGG ATC GAG ATC Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile 80 85 90	1010
AAG GAC ACC AAG GAA GCT TTA GAC AAG ATA GAG GAA GAG CAA AAC AAG Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys 95 100 105 110	1058
TCC AAG AAG AAG GCC CAG CAG GCA GCA GCT GAC ACA GGA CAC AGC AAT Ser Lys Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn 111 115 120 125	1106
CAG GTC AGC CAA AAT TAC CCT ATA GTG CAG AAC ATC CAG GGG CAA ATG Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met 130 135 140	1154
GTA CAT CAG GCC ATA TCA CCT AGA ACT TTA AAT GCA TGG GTA AAA GTA Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val 145 150 155	1202
GTA GAA GAG AAG GCT TTC AGC CCA GAA GTG ATA CCC ATG TTT TCA GCA Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala 160 165 170	1250
TTA TCA GAA GGA GCC ACC CCA CAG GAC CTG AAC ACG ATG TTG AAC ACC Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr 175 180 185 190	1298
GTG GGG GGA CAT CAA GCA GCC ATG CAA ATG TTA AAA GAG ACC ATC AAT Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn 195 200 205	1346
GAG GAA GCT GCA GAA TGG GAT AGA GTG CAT CCA GTG CAT GCA GGG CCT Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro 210 215 220	1394
ATT GCA CCA GGC CAG ATG AGA GAA CCA AGG GGA AGT GAC ATA GCA GGA Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly 225 230 235	1442
ACT ACT AGT ACC CTT CAG GAA CAA ATA GGA TGG ATG ACA AAT AAT CCA Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro 240 245 250	1490
CCT ATC CCA GTA GGA GAG ATC TAC AAG AGG TGG ATA ATC CTG GGA TTG Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu 255 260 265 270	1538
AAC AAG ATC GTG AGG ATG TAT AGC CCT ACC AGC ATT CTG GAC ATA AGA Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg 275 280 285	1586
CAA GGA CCA AAG GAA CCC TTT AGA GAC TAT GTA GAC CGG TTC TAT AAA Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys 290 295 300	1634
ACT CTA AGA GCT GAG CAA GCT TCA CAG GAG GTA AAA AAT TGG ATG ACA	1682

Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr	
305 310 315	
GAA ACC TTG TTG GTC CAA AAT GCG AAC CCA GAT TGT AAG ACC ATC CTG	1730
Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu	
320 325 330	
AAG GCT CTC GGC CCA GCG GCT ACA CTA GAA GAA ATG ATG ACA GCA TGT	1778
Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys	
335 340 345 350	
CAG GGA GTA GGA GGA CCC GGC CAT AAG GCA AGA GTT TTG TAG	1820
Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val Leu	
355 360	
GGATCCACTA GTTCTAGACT CGAGGGGGGG CCCGGTACCT TTAAGACCAA TGACTTACAA	1880
GGCAGCTGTA GATCTTAGCC ACTTTTAAA AGAAAAGGGG GGACTGGAAG GGCTAATTCA	1940
CTCCCAAAGA AGACAAGATA TCCTTGATCT GTGGATCTAC CACACACAAG GCTACTTCCC	2000
TGATTGGCAG AACTACACAC CAGGGCCAGG GGTGAGATAT CCACTGACCT TTGGATGGTG	2060
CTACAAGTA GTACCAAGTTG AGCCAGATAA GGTAGAAGAG GCCAATAAAG GAGAGAACAC	2120
CAGCTTGTTA CACCCTGTGA GCCTGCATGG AATGGATGAC CCTGAGAGAG AAGTGTAGA	2180
GTGGAGGTTT GACAGCCGCC TAGCATTTC A CACGTGGCC CGAGAGCTGC ATCCGGAGTA	2240
CTTCAAGAAC TGCTGACATC GAGCTTGCTA CAAGGGACTT TCCGCTGGGG ACTTTCAGG	2300
GAGGCGTGGC CTGGGCGGGA CTGGGGAGTG GCGAGCCCTC AGATGCTGCA TATAAGCAGC	2360
TGCTTTTTCG CTGFACTGGG TCTCTCTGGT TAGACCAGAT CTGAGCCTGG GAGCTCTCTG	2420
GCTAACTAGG GAACCCACTG CTTAAGCCTC AATAAAGCTT GCCTTGAGTG CTTCAAGTAG	2480
TGTGTGCCCG TCTGTTGTGT GACTCTGGTA ACTAGAGATC CCTCAGACCC TTTTAGTCAG	2540
TGTGGAATAT CTCTAGCACC CCCAGGAGG TAGAGGTTGC AGTGAGCCAA GATCGCGCCA	2600
CTGCATTCCA GCCTGGGCAA GAAAACAAGA CTGTCTAAAA TAATAATAAT AAGTTAAGGG	2660
TATTAATAT ATTTATACAT GGAGGTCATA AAAATATATA TATTTGGGCT GGGCGCAGTG	2720
GCTCACACCT GCGCCCGGCC CTTTGGGAGG CCGAGGCAGG TGGATCACCT GAGTTTGGGA	2780
GTTCAGACC AGCCTGACCA ACATGGAGAA ACCCCTTCTC TGTGTATTTT TAGTAGATT	2840
TATTTTATGT GTATTTTATT CACAGGTATT TCTGGAAAAC TGAACTGTT TTTCTCTAC	2900
TCTGATACCA CAAGAATCAT CAGCACAGAG GAAGACTTCT GTGATCAAAAT GTGGTGGGAG	2960
AGGGAGGTTT TCACCAGCAC ATGAGCAGTC AGTTCTGCCG CAGACTCGGC GGGTGTCTT	3020
CGGTTTCAGTT CCAACACCGC CTGCCTGGAG AGAGGTCAGA CCACAGGGTG AGGGCTCAGT	3080
CCCCAAGACA TAAACACCCA AGACATAAAC ACCCAACAGG TCCACCCCGC CTGCTGCCCCA	3140
GGCAGAGCCG ATTCACCAAG ACGGGAATTA GGATAGAGAA AGAGTAAGTC ACACAGAGCC	3200
GGCTGTGCGG GAGAACGGAG TTCTATTATG ACTCAAAATCA GTCTCCCCAA GCATTCGGGG	3260
ATCAGAGTTT TTAAGGATAA CTTAGTGTGT AGGGGGCCAG TGAGTTGGAG ATGAAAGCGT	3320
AGGGAGTCGA AGGTGTCCTT TTGCGCCGAG TCAGTTCCTG GGTGGGGGCC ACAAGATCGG	3380
ATGAGCCAGT TTATCAATCC GGGGGTGCCA GCTGATCCAT GGAGTGCAGG GTCTGCAAAA	3440
TATCTCAAGC ACTGATTGAT CTTAGGTTTT ACAATAGTGA TGTTACCCCA GGAACAATTT	3500

GGGGAAGGTC AGAATCTTGT AGCCTGTAGC TGCATGACTC CTAAACCATA ATTTCTTTTT	3560
TGTTTTTTTT TTTTATTTT TGAGACAGGG TCTCACTCTG TCACCTAGGC TGGAGTGCAG	3620
TGGTGCAATC ACAGCTCACT GCAGCCCTA GAGCGGCCG CACCGCGGTG GAGCTCCAAT	3680
TCGCCCTATA GTGAGTCGTA TTACAATTCA CTGGCCGTCG TTTTACAACG TCGTGA CTGG	3740
GAAACCCTG GCGTTACCCA ACTTAATCGC CTTGCAGCAC ATCCCCCTT CGCCAGCTGG	3800
CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCAAC AGTTGCGCAG CCTGAATGGC	3860
GAATGGCGCG AATTGTAAA CGTTAATATT TTGTAAAAT TCGCGTAAA TTTTGTAA	3920
ATCAGCTCAT TTTTAAACA ATAGGCCGAA ATCGGCAAAA TCCCTTATA ATCAAAAGAA	3980
TAGACCAGA TAGGGTTGAG TGTGTTCCA GTTGGAACA AGAGTCCACT ATTAAGA AAC	4040
GTGGA CTCCA ACGTCAAAGG GCGAAAAACC GTCTATCAGG GCGATGGCCC ACTACGTGAA	4100
CCATACCCT AATCAAGTTT TTTGGGGTCG AGGTGCCGTA AAGCACTAAA TCGGAACCTT	4160
AAAGGGAGCC CCCGATTTAG AGCTTGACGG GGAAAGCCGG CGAACGTGGC GAGAAAGGAA	4220
GGGAAGAAAG CGAAAGGAGC GGGCGCTAGG GCGCTGGCAA GTGTAGCGGT CACGCTGCGC	4280
GTAACCAACA CACCCGCCGC GCTTAATGCG CCGCTACAGG GCGCGTCCA GGTGGCACTT	4340
TTGGGGAAA TGTGCGCGGA ACCCTATTT GTTTATTTT CTAAATACAT TCAATATGT	4400
ATCCGCTCAT GAGACAATAA CCCTGATAAA TGCTTCAATA ATATTGAAAA AGGAAGAGTA	4460
TGAGTATTCA ACATTTCCGT GTCGCCCTTA TTCCCTTTTT TGCGGCATTT TGCCTTCCTG	4520
TTTTTGCTCA CCCAGAAACG CTGGTGAAAG TAAAAGATGC TGAAGATCAG TTGGGTGCAC	4580
GAGTGGGTTA CATCGAACTG GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTGCCCCG	4640
AAGAACGTTT TCCAATGATG AGCACTTTTA AAGTTCGTCT ATGTGGCGCG GTATTATCCC	4700
GTATTGACGC CGGGCAAGAG CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTTGG	4760
TTGAGTACTC ACCAGTCACA GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT	4820
GCAGTGCTGC CATAACCATG AGTGATAACA CTGCGGCCAA CTTACTTCTG ACAACGATCG	4880
GAGGACCGAA GGAGCTAACC GCTTTTTTGC ACAACATGGG GGATCATGTA ACTCGCCTTG	4940
ATCGTTGGGA ACCGGAGCTG AATGAAGCCA TACCAAACGA CGAGCGTGAC ACCACGATGC	5000
CTGTAGCAAT GGCAACAACG TTGCGCAAAC TATTAAGTGG CGAACTACTT ACTCTAGCTT	5060
CCCGGCAACA ATTAATAGAC TGGATGGAGG CGGATAAAGT TGCAGGACCA CTTCTGCGCT	5120
CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG AGCCGGTGAG CGTGGGTCTC	5180
GCGGTATCAT TGCAGCACTG GGGCCAGATG GTAAGCCCTC CCGTATCGTA GTTATCTACA	5240
CGACGGGGAG TCAGGCAACT ATGGATGAAC GAAATAGACA GATCGCTGAG ATAGGTGCCT	5300
CACTGATTAA GCATTGGTAA CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT	5360
TAAAAC TTCA TTTTAAATTT AAAAGGATCT AGGTGAAGAT CCTTTTGTAT AATCTCATGA	5420
CCAAAATCCC TTAACGTGAG TTTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA	5480
AAGGATCTTC TTGAGATCCT TTTTCTGTC GCGTAATCTG CTGCTTGCAA ACAAAAAAAC	5540
CACCGCTACC AGCGGTGGTT TGTGTCGGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG	5600
TAACTGGCTT CAGCAGAGCG CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG	5660

GCCACCACTT CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC	5720
CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG GTTGGACTCA AGACGATAGT	5780
TACCGGATAA GCGGCAGCGG TCGGGCTGAA CGGGGGGTTC GTGCACACAG CCCAGCTTGG	5840
AGCGAACGAC CTACACCGAA CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC	5900
TTCCCGAAGG GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC	5960
GCACGAGGGA GCTTCCAGGG GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC	6020
ACCTCTGACT TGAGCGTCGA TTTTGTGAT GCTCGTCAGG GGGGCGGAGC CTATGGAAAA	6080
ACGCCAGCAA CGCGGCCTTT TTACGGTTCC TGGCCTTTTG CTGGCCTTTT GCTCACATGT	6140
TCTTTCCTGC GTTATCCCTT GATTCTGTGG ATAACCGTAT TACCGCCTTT GAGTGAGCTG	6200
ATACCGCTCG CCGCAGCCGA ACGACCGAGC GCAGCGAGTC AGTGAGCGAG GAAGCGGAAG	6260
AGCGCCCAAT ACGCAAACCG CCTCTCCCCG CGCGTTGGCC GATTCAATTA TGCAGCTGGC	6320
ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAT GTGAGTTAGC	6380
TCACTCATTG GGCACCCAGG GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA	6440
TTGTGAGCGG ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GCCAAGCTCG	6500
GAATTAACCC TACTAAAGG GAACAAAAGC TGCTGCAGGG TCCCTAACTG CCAAGCCCCA	6560
CAGTGTGCCC TGAGGCTGCC CCTTCCTTCT AGCGGCTGCC CCCACTCGGC TTTGCTTTCC	6620
CTAGTTTCAG TTACTTGCCT TCAGCCAAGG TCTGAAACTA GGTGCGCACA GAGCGGTAAG	6680
ACTGCGAGAG AAAGAGACCA GCTTTACAGG GGGTTTATCA CAGTGCACCC TGACAGTCGT	6740
CAGCCTCACA GGGGGTTTAT CACATTGCAC CCTGACAGTC GTCAGCCTCA CAGGGGGTTT	6800
ATCACAGTGC ACCCTTACAA TCATTCCATT TGATTACAA TTTTTTTAGT CTCTACTGTG	6860
CCTAACTTGT AAGTTAAATT TGATCAGAGG TGTGTTCCCA GAGGGGAAAA CAGTATATAC	6920
AGGGTTCAGT ACTATCGCAT TTCAGGCCTC CACCTGGGTC TTGGAATGTG TCCCCGAGG	6980
GGTGATGACT ACCTCAGTTG GATCTCCACA GGTCACAGTG ACACAAGATA ACCAAGACAC	7040
CTCCCAAGGC TACCACAATG GGCCGCCCTC CACGTGCACA TGCCCGGAGG AACTGCCATG	7100
TCGGAGGTGC AAGCACACCT GCGCATCAGA GTCCTTGGTG TGGAGGGAGG GACCAGCGCA	7160
GCTTCCAGCC ATCCACCTGA TGAACAGAAC CTAGGGAAGG CCCCAGTTCT ACTTACACCA	7220
GGAAAGGC	7228

(131) INFORMATION FOR SEQ ID NO: 130:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 AMINO ACIDS
(B) TYPE: AMINO ACID
(C) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130

Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly	Gly	Glu	Leu	Asp	Arg	Trp
1				5					10					15	

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
 20 25 30
 His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
 35 40 45
 Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
 50 55 60
 Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
 65 70 75 80
 Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
 85 90 95
 Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
 100 105 110
 Lys Lys Ala Gln Gln Ala Ala Asp Thr Gly His Ser Asn Gln Val
 115 120 125
 Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
 130 135 140
 Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
 145 150 155 160
 Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
 165 170 175
 Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
 180 185 190
 Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
 195 200 205
 Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
 210 215 220
 Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
 225 230 235 240
 Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
 245 250 255
 Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
 260 265 270
 Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
 275 280 285
 Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
 290 295 300
 Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
 305 310 315 320
 Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
 325 330 335
 Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
 340 345 350
 Val Gly Gly Pro Gly His Lys Ala Arg Val Leu
 355 360